

- a. contacting the sample with a Complex under conditions whereby said Complex can bind to the Target Nucleic Acid to form a Complex-Target Nucleic Acid hybrid, wherein said Complex comprises:
- i. a first nucleic acid comprising, from 3' to 5': a Substrate Hybridization Domain and a Signal Template Domain, wherein:
 - (1) the Substrate Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides; and
 - (2) the Signal Template Domain comprises a sequence of about 5 to about 100 nucleotides;and:
 - ii. a second nucleic acid comprising from 3' to 5': a Signal Domain, a Template Hybridization Domain and a Target Binding Domain, wherein:
 - (1) the Signal Domain comprises a sequence of about 5 to about 100 nucleotides, which sequence shows complementarity toward and is hybridizable to the Signal Template Domain of the first nucleic acid, and of which at least two nucleotides are detectably labeled;
 - (2) the Template Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first nucleic acid;
 - (3) the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the Template Hybridization Domain;and
- b. detecting any Complex-Target Nucleic Acid hybrids, so that if a Complex-Target Nucleic Acid hybrid is detected, a Target Nucleic Acid is detected in the sample.

50. (Amended) A method for detecting a Target Nucleic Acid in a sample, comprising:
- a. dissociating a Complex to generate a single stranded first nucleic acid and a single stranded second nucleic acid, wherein said complex comprises:
 - i. a first nucleic acid comprising, from 3' to 5': a Substrate Hybridization Domain and a Signal Template Domain, wherein:
 - (1) the Substrate Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides; and
 - (2) the Signal Template Domain comprises a sequence of about 5 to about 100 nucleotides;and:
 - ii. a second nucleic acid comprising from 3' to 5': a Signal Domain, a Template Hybridization Domain and a Target Binding Domain, wherein:
 - (1) the Signal Domain comprises a sequence of about 5 to about 100 nucleotides, which sequence shows complementarity toward and is hybridizable to the Signal Template Domain of the first nucleic acid, and of which at least two nucleotides are detectably labeled;
 - (2) the Template Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first nucleic acid;
 - (3) the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the Template Hybridization Domain;
 - b. contacting the sample with the second nucleic acid of step a. under conditions whereby said second nucleic acid can bind to the Target Nucleic Acid to form a second nucleic acid-Target Nucleic Acid hybrid; and

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- c. detecting any second nucleic acid-Target Nucleic Acid hybrids, so that if a second nucleic acid-Target Nucleic Acid hybrid is detected, a Target Nucleic Acid is detected in the sample.

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51. (Amended) A kit for labeling a nucleic acid molecule, comprising a reaction mixture and a DNA polymerase, wherein the reaction mixture comprises:
- a. a first nucleic acid comprising, from 3' to 5': a Substrate Hybridization Domain and a Signal Template Domain, wherein:
 - i. the Substrate Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides; and
 - ii. the Signal Template Domain comprises a sequence of about 5 to about 100 nucleotides;and:
 - b. a second nucleic acid comprising from 3' to 5': a Template Hybridization Domain and a Target Binding Domain, wherein:
 - i. the Template Hybridization Domain comprises a sequence of about 5 to about 20 nucleotides, is not detectably labeled, and shows complementarity toward and is hybridizable to the Substrate Hybridization Domain of the first nucleic acid;
 - ii. the Target Binding Domain is not detectably labeled and comprises a nucleotide sequence heterologous to that of the Template Hybridization Domain.
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Please add the following new claims:

55. (New) The method of claim 29, wherein the Probe has a specific activity of at least 7×10^7 CPM per picomole, and wherein the Probe comprises the Target Binding Domain, the Template Hybridization Domain and the Signal Domain.

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56. (New) The method of claim 29, wherein the Probe has a specific activity of at least 9×10^7 CPM per picomole, and wherein the Probe comprises the Target Binding Domain, the Template Hybridization Domain and the Signal Domain.